FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000
Please cite:
W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaFAA4GaWRi: 704 aa
>SEQ ID NO:2
vs /tmp/fastaGAA5GaWRi library
searching /tmp/fastaGAA5GaWRi library

704 residues in   1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 38, opt: 26, gap-pen: -12/ -2, width: 16
Scan time: 0.033 .
The best scores are: opt
gi|12583612|emb|CAC27329.1| neurolysin [Homo sapi   (704) 4666

>>gi|12583612|emb|CAC27329.1| neurolysin [Homo sapiens]
  (704 aa)
 initn: 4666 init1: 4666 opt: 4666
Smith-Waterman score: 4666; 100.000% identity in 704 aa overlap (1-704:1-704)

```
              10        20        30        40        50        60
SEQ     MIARCLLAVRSLRRVGGSRILLRMTLGREVMSPLQAMSSYTVAGRNVLRWDLSPEQIKTR
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125  MIARCLLAVRSLRRVGGSRILLRMTLGREVMSPLQAMSSYTVAGRNVLRWDLSPEQIKTR
              10        20        30        40        50        60

              70        80        90       100       110       120
SEQ     TEELIVQTKQVYDAVGMLGIEEVTYENCLQALADVEVKYIVERTMLDFPQHVSSDKEVRA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125  TEELIVQTKQVYDAVGMLGIEEVTYENCLQALADVEVKYIVERTMLDFPQHVSSDKEVRA
              70        80        90       100       110       120

             130       140       150       160       170       180
SEQ     ASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYLEKSIKMGKRNGLHL
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125  ASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYLEKSIKMGKRNGLHL
             130       140       150       160       170       180

             190       200       210       220       230       240
SEQ     PEQVQNEIKSMKKRMSELCIDFNKNLNEDDTFLVFSKAELGALPDDFIDSLEKTDDDKYK
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125  PEQVQNEIKSMKKRMSELCIDFNKNLNEDDTFLVFSKAELGALPDDFIDSLEKTDDDKYK
             190       200       210       220       230       240

             250       260       270       280       290       300
SEQ     ITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKEENTIILQQLLPLRTKVAKLLGYSTHA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125  ITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKEENTIILQQLLPLRTKVAKLLGYSTHA
             250       260       270       280       290       300

             310       320       330       340       350       360
SEQ     DFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKECKDRGFEYDGKINAWD
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125  DFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKECKDRGFEYDGKINAWD
             310       320       330       340       350       360

             370       380       390       400       410       420
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SEQ     LYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTL
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125  LYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTL
            370       380       390       400       410       420


            430       440       450       460       470       480
SEQ     YTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMAVAALVVNFSQPV
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125  YTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMAVAALVVNFSQPV
            430       440       450       460       470       480


            490       500       510       520       530       540
SEQ     AGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLENWVWDVD
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125  AGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLENWVWDVD
            490       500       510       520       530       540


            550       560       570       580       590       600
SEQ     SLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEY
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125  SLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEY
            550       560       570       580       590       600


            610       620       630       640       650       660
SEQ     AKYCSEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPE
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125  AKYCSEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPE
            610       620       630       640       650       660


            670       680       690       700
SEQ     VGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGLHAP
        :::::::::::::::::::::::::::::::::::::::::::::
|125    VGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGLHAP
            670       680       690       700
```

704 residues in 1 query   sequences
704 residues in 1 library sequences
 Scomplib [version 3.3t05 March 30, 2000]
 start: Fri Nov 1 15:59:40 2002 done: Fri Nov 1 15:59:41 2002
 Scan time: 0.033 Display time: 0.700

Function used was FASTA